

Title Genomics approaches for better understanding the biological basis of fruit ripening and quality  
Authors P. Tonutti and C. Bonghi  
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### **Abstract**

Genomics tools are nowadays commonly used in many plant science labs and are rapidly spreading for studying transcriptome profiles throughout fruit development and discovering new genes involved in processes modulating quality traits. In fact, transcript profiling (TP) has the potential to reveal transcriptional hierarchy during development for thousands of genes, as well as providing expression data for many genes of unknown or putative function. By using both direct and indirect TP methods, a body of new information is now available concerning ripening regulation in both climacteric and non-climacteric fruits, and a number of genes differentially expressed during the transition from unripe to ripe fruit and related to the evolution of quality parameters have been identified. Concerning direct TP methods, isolated ESTs have been used for digital expression analysis throughout fruit development in several fruit species and for comparative genomics investigations. The comparative approach has allowed to identify genes putatively encoding transcription factors induced at ripening in both grapes and peaches indicating that some regulatory elements are in common in non-climacteric and climacteric fruits. Among direct TP analyses, cDNA-AFLP has been widely used in several fruit types including grape berry: using this technique, we have identified 92 and 82 genes differentially regulated in skins of grape berries during extended ripening off- (detachment) and on- (late harvest) plant, respectively. Some of these genes are in common but others are specifically induced or repressed by each treatment and may be responsible for some quality traits characterizing late-harvest or partially dehydrated grape berries. Considering the indirect analyses, the first peach microarray ( $\mu$ PEACH 1.0) containing oligo-probes corresponding to 4806 unigenes has been constructed and used for comparing transcriptome of pre-climacteric and climacteric peach fruit: 267 and 109 genes appear up- and down-regulated, respectively, during this transition. Among these, genes responsible for typical peach fruit traits (pulp pigmentation) and others, already associated to ripening in other species, but never studied in peach have been identified.